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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=8; day=5; hr=16; min=35; sec=37; ms=897;]

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Reviewer Comments:

<210> 2

<211> 1588

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(1059)

<400> 2

atg gag ggg atc agt ata tac act tca gat aac tac acc gag gaa 45

Per the above sequence id# 2 is invalid, please insert (3) letter
codings for amino acids immediately below
corresponding nucleotide triplets. This error is seen globally
throughout the sequence.

<210> 5

<211> 89

<212> PRT

<213> Artificial Sequence

<220>

<223> Ligand peptide

<210> 9

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> added peptide

Per the above, both <223> responses for sequence id#'s 5 and 9 are invalid, please explain Artificial.

Application No: 10785230 Version No: 2.0

Input Set:

Output Set:

Started: 2008-06-26 16:28:54.530
Finished: 2008-06-26 16:28:55.423
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 893 ms
Total Warnings: 12
Total Errors: 0
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

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SEQUENCE LISTING

<110> KISHIMOTO, Tadimitsu
 NAGASAWA, Takashi
 TACHIBANA, Kazunobu

<120> Inhibiting vascularization using antibodies to CXCR4 and SDF-1

<130> 46124-5042-US01

<140> 10785230

<141> 2004-02-25

<150> US 09/646,785

<151> 2001-02-16

<150> PCT/JP99/01448

<151> 1999-03-23

<150> JP10/95448

<151> 1998-03-24

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<220>
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 <222> (1) ... (1059)

<400> 2

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tcc atc atc ttc tta act ggc att gtg ggc aat gga ttg gtc atc 180
ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag 225
tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg 270
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ctg ctg act att ccc gac ttc atc ttt gcc aac gtc agt gag gca 540
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gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
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aca gtc atc ctc atc ctg gct ttc ttc gcc tgt tgg ctg cct tac 765
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aag caa ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc 855
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<212> PRT
<213> Mus

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<400> 3

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Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu
      50              55              60
Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr
      65              70              75
Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val
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Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp Trp Tyr
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Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val
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Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
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Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg
      140             145             150
Lys Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro
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Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser
      170             175             180
Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg
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Phe	Lys	Ser	Ser	Ala	Gln	His	Ala	Leu	Asn	Ser	Met	Ser	Arg	Gly	
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Ser	Ser	Leu	Lys	Ile	Leu	Ser	Lys	Gly	Lys	Arg	Gly	Gly	His	Ser	
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<211> 1758

<212> DNA

<213> Mus

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<222> (1)...(1080)

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gtg atc ctg gtc atg ggt tac cag aag aag cta agg agc atg acg 225
gac aag tac cgg ctg cac ctg tca gtg gct gac ctc ctc ttt gtc 270
atc aca ctc ccc ttc tgg gca gtt gat gcc atg gct gac tgg tac 315
ttt ggg aaa ttt ttg tgt aag gct gtc cat atc atc tac act gtc 360
aac ctc tac agc agc gtt ctc atc ctg gcc ttc atc agc ctg gac 405
cgg tac ctc gcc att gtc cac gcc acc aac agt caa agg cca agg 450
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cag ggg gac atc agt cag ggg gat gac agg tac atc tgt gac cgc 585
ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc cag cat 630
ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc tgt 675
tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac cag 720
aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc 765
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<211> 89

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<213> Artificial Sequence

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<223> Ligand peptide

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Pro	Cys	Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys
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Ala	Arg	Leu	Lys	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	
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<213> Mus

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<222> (471)...(743)

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gcc cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aag						698
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<212> PRT
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<211> 1781
<212> DNA
<213> Mus

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<220>
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<222> (82)...(351)

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81

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gca cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aaa 306
tta aag tgg atc caa gag tac ctg gag aaa gct tta aac aag taa 351
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